



# results of BLAST

## BLASTN 2.2.5 [Nov-16-2002]

### Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1041886212-011034-25435

### Query=

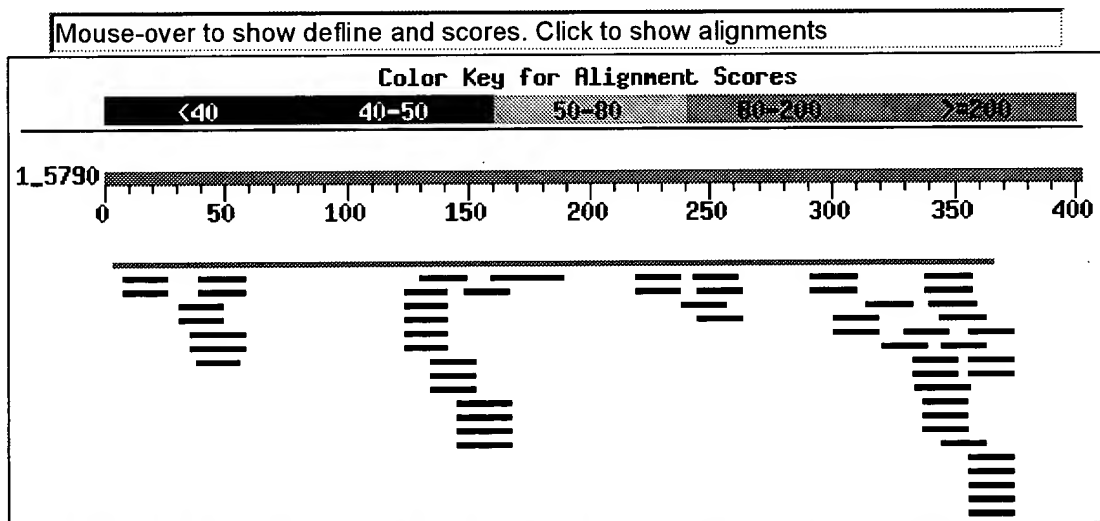
(402 letters)

**Database:** All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, or phase 0, 1 or 2 HTGS sequences)  
1,561,220 sequences; 7,640,351,724 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)






## Distribution of 58 Blast Hits on the Query Sequence



Sequences producing significant alignments:

Score E  
(bits) Value

<a href="#">gi 21213184 gb AY109457.1 </a>	Zea mays CL12356_1 mRNA sequence	<u>250</u>	1e-63
<a href="#">gi 26892321 gb AC091230.23 </a>	Homo sapiens chromosome 15, clo...	<u>40</u>	2.4
<a href="#">gi 12002009 gb AF063186.1 AF063186</a>	Arthrobacter paraffineus...	<u>40</u>	2.4
<a href="#">gi 27368269 emb AL731822.31 </a>	Mouse DNA sequence from clone ...	<u>40</u>	2.4

<a href="#">gi 24430304 emb AL928751.2 CNS08CBO</a>	<a href="#">Oryza sativa chromosome...</a>	<a href="#">40</a>	2.4	
<a href="#">gi 2981261 gb AC004149.1 AC004149</a>	<a href="#">Homo sapiens chromosome 1...</a>	<a href="#">40</a>	2.4	
<a href="#">gi 8573811 emb AL138761.12 </a>	<a href="#">Human DNA sequence from clone R...</a>	<a href="#">40</a>	2.4	
<a href="#">gi 1825501 gb U76577.1 HUMCOL14</a>	<a href="#">Human 180 kDa bullous pemph...</a>	<a href="#">40</a>	2.4	
<a href="#">gi 2879763 emb Z97209.1 SPAC19G12</a>	<a href="#">S.pombe chromosome I cosm...</a>	<a href="#">40</a>	2.4	
<a href="#">gi 13359356 dbj AP001980.5 </a>	<a href="#">Homo sapiens genomic DNA, chrom...</a>	<a href="#">40</a>	2.4	
<a href="#">gi 13359355 dbj AP001883.5 </a>	<a href="#">Homo sapiens genomic DNA, chrom...</a>	<a href="#">40</a>	2.4	
<a href="#">gi 24796750 gb AC090646.2 </a>	<a href="#">Homo sapiens chromosome 3 clone ...</a>	<a href="#">38</a>	9.5	
<a href="#">gi 20340420 gb AC112485.4 </a>	<a href="#">Homo sapiens 3 BAC RP11-776B11 (...)</a>	<a href="#">38</a>	9.5	
<a href="#">gi 25990260 gb AC091182.5 </a>	<a href="#">Homo sapiens chromosome 8, clone...</a>	<a href="#">38</a>	9.5	
<a href="#">gi 25901147 gb AC124483.4 </a>	<a href="#">Mus musculus chromosome 5 clone ...</a>	<a href="#">38</a>	9.5	
<a href="#">gi 22539419 gb AC112144.4 </a>	<a href="#">Mus musculus chromosome 19 clone...</a>	<a href="#">38</a>	9.5	
<a href="#">gi 22539095 gb AC094105.3 </a>	<a href="#">Homo sapiens chromosome 5 clone ...</a>	<a href="#">38</a>	9.5	
<a href="#">gi 22417370 gb AC116035.2 </a>	<a href="#">Homo sapiens chromosome 3 clone ...</a>	<a href="#">38</a>	9.5	
<a href="#">gi 22325763 ref NM_127468.2 </a>	<a href="#">Arabidopsis thaliana chromosom...</a>	<a href="#">38</a>	9.5	
<a href="#">gi 21743758 gb AC010331.8 </a>	<a href="#">Homo sapiens chromosome 19 clone...</a>	<a href="#">38</a>	9.5	
<a href="#">gi 21553249 gb AC116991.2 </a>	<a href="#">Homo sapiens chromosome 3 clone ...</a>	<a href="#">38</a>	9.5	
<a href="#">gi 21281482 gb AC108130.2 </a>	<a href="#">Homo sapiens chromosome 5 clone ...</a>	<a href="#">38</a>	9.5	
<a href="#">gi 20800407 gb AC110089.5 </a>	<a href="#">Homo sapiens BAC clone RP11-806P...</a>	<a href="#">38</a>	9.5	
<a href="#">gi 21240691 gb AC116359.2 </a>	<a href="#">Homo sapiens chromosome 5 clone ...</a>	<a href="#">38</a>	9.5	
<a href="#">gi 20907729 gb AE013562.1 </a>	<a href="#">Methanosarcina mazei strain Goel...</a>	<a href="#">38</a>	9.5	
<a href="#">gi 20466062 gb AY096796.1 </a>	<a href="#">Arabidopsis thaliana At2g19110/T...</a>	<a href="#">38</a>	9.5	
<a href="#">gi 20143840 gb AC108153.4 </a>	<a href="#">Homo sapiens BAC clone RP11-512B...</a>	<a href="#">38</a>	9.5	
<a href="#">gi 20196928 gb AC002392.3 </a>	<a href="#">Arabidopsis thaliana chromosome ...</a>	<a href="#">38</a>	9.5	
<a href="#">gi 19570160 gb AC104302.2 </a>	<a href="#">Homo sapiens chromosome 3 clone ...</a>	<a href="#">38</a>	9.5	
<a href="#">gi 19071217 gb AF412407.1 </a>	<a href="#">Arabidopsis thaliana putative he...</a>	<a href="#">38</a>	9.5	
<a href="#">gi 18543162 gb AC093389.6 </a>	<a href="#">Homo sapiens BAC clone RP11-669N...</a>	<a href="#">38</a>	9.5	
<a href="#">gi 18093040 gb AC004953.2 </a>	<a href="#">Homo sapiens PAC clone RP5-1059M...</a>	<a href="#">38</a>	9.5	
<a href="#">gi 13677114 gb AC016674.9 </a>	<a href="#">Homo sapiens BAC clone RP11-36C8...</a>	<a href="#">38</a>	9.5	
<a href="#">gi 14277274 gb AC021079.4 AC021079</a>	<a href="#">Homo sapiens chromosome ...</a>	<a href="#">38</a>	9.5	
<a href="#">gi 10881111 gb AC051663.9 AC051663</a>	<a href="#">Homo sapiens BAC clone R...</a>	<a href="#">38</a>	9.5	
<a href="#">gi 13794247 gb AC044817.5 AC044817</a>	<a href="#">Homo sapiens, clone RP11...</a>	<a href="#">38</a>	9.5	
<a href="#">gi 13357222 gb AC090884.1 AC090884</a>	<a href="#">Homo sapiens chromosome ...</a>	<a href="#">38</a>	9.5	
<a href="#">gi 11024922 gb AC011194.15 AC011194</a>	<a href="#">Mus musculus chromosome...</a>	<a href="#">38</a>	9.5	
<a href="#">gi 12061558 gb AC019233.7 AC019233</a>	<a href="#">Homo sapiens clone RP11-...</a>	<a href="#">38</a>	9.5	
<a href="#">gi 25136716 emb AL928804.5 </a>	<a href="#">Mouse DNA sequence from clone R...</a>	<a href="#">38</a>	9.5	
<a href="#">gi 11990206 emb AJ297264.1 ATH297264</a>	<a href="#">Arabidopsis thaliana m...</a>	<a href="#">38</a>	9.5	
<a href="#">gi 4874262 gb AC007590.1 AC007590</a>	<a href="#">Homo sapiens BAC 161A6, c...</a>	<a href="#">38</a>	9.5	
<a href="#">gi 23040001 ref NZ_AAAU01000006.1 </a>	<a href="#">Trichodesmium erythraeum...</a>	<a href="#">38</a>	9.5	
<a href="#">gi 1934877 emb Z82211.1 HS447N6</a>	<a href="#">Human DNA sequence from PAC...</a>	<a href="#">38</a>	9.5	
<a href="#">gi 16904687 dbj AP003450.3 </a>	<a href="#">Oryza sativa (japonica cultivar...</a>	<a href="#">38</a>	9.5	
<a href="#">gi 16214543 emb AL158044.17 </a>	<a href="#">Human DNA sequence from clone ...</a>	<a href="#">38</a>	9.5	
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<a href="#">gi 2618600 dbj AB008265.1 </a>	<a href="#">Arabidopsis thaliana genomic DNA...</a>	<a href="#">38</a>	9.5	
<a href="#">gi 21425606 emb AL714006.13 </a>	<a href="#">Mouse DNA sequence from clone ...</a>	<a href="#">38</a>	9.5	
<a href="#">gi 21655409 emb AL713983.9 </a>	<a href="#">Mouse DNA sequence from clone R...</a>	<a href="#">38</a>	9.5	
<a href="#">gi 19571951 emb AL606824.13 </a>	<a href="#">Mouse DNA sequence from clone ...</a>	<a href="#">38</a>	9.5	
<a href="#">gi 4579991 dbj AP000070.1 </a>	<a href="#">Homo sapiens genomic DNA, chromo...</a>	<a href="#">38</a>	9.5	

## Alignments

>gi|21213184|gb|AY109457.1| Zea mays CL12356\_1 mRNA sequence  
Length = 1349

Score = 250 bits (126), Expect = 1e-63  
Identities = 316/366 (86%), Gaps = 10/366 (2%)  
Strand = Plus / Minus

Query: 5 gccgggctcaccagctggcccagtgaaggcttaaag-acatgtgccaggagaaggggcct 63  
|||||  
Sbjct: 496 gccgggctcaccagctggtccag-gaaggcttaaagtacatgttccaggagaaggg-cct 439

Query: 64 tgaacttgtgtggtctgcacccctaattattgct-cagatgtggcaatggagcttctatat 122  
||| |||||  
Sbjct: 438 tgtaacttgtgtggtctgcaccc-aattattgctacagatgtggcaatgtagcttctatat 380


Query: 123 taagcttcgatgagaagaaggaaaggagatgtcaaggtcttcacagagaccgaggaaaac 182  
|||||  
Sbjct: 379 taagcttcgatgagaagatggaaa-gagatgtcaaggtcttcacagagacagaggaaaac 321

Query: 183 aaccagattccagggcccaagggttgaatcccatatttcctttgacttcaggtggacaa 242  
||||| ||| ||||| ||| ||| |||||  
Sbjct: 320 aaccagatgcgaggcccaaggac-tgcagtcccatatttcctctgacttcaattgtac-a 263

Query: 243 ttttagaaggcaatatttaaatctggaaggggtaaagaacaatcagatggtgttaat-tg 301  
||||| ||| ||||| ||||| ||||| ||| ||||| ||||| |||  
Sbjct: 262 ttttagaagtcaacattttaaatctgtaagggttaaagatcagtcagat-gtgtttatcat 204

Query: 302 tggaggttcagatcataatgccatctgatgcattccatttctggtttctttgaacacaa 361  
|| ||||| ||||| ||| ||||| ||||| ||| ||||| ||||| |||  
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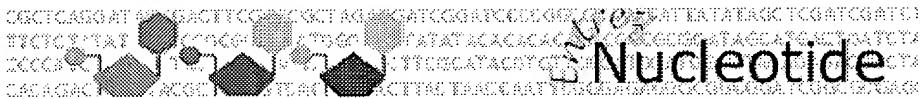
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|||||  
Sbjct: 143 gtacaa 138

>gi|26892321|gb|AC091230.23|  Homo sapiens chromosome 15, clone RP11-414J4, comple  
Length = 206482

Score = 40.1 bits (20), Expect = 2.4  
Identities = 20/20 (100%)  
Strand = Plus / Minus

Query: 131 gatgagaagaaggaaaggag 150  
|||||  
Sbjct: 50697 gatgagaagaaggaaaggag 50678

>gi|12002009|gb|AF063186.1|AF063186 Arthrobacter paraffineus DNA polymerase I gene,

[PubMed](#)   [Nucleotide](#)   [Protein](#)   [Genome](#)   [Structure](#)   [PMC](#)   [Taxonomy](#)   [OMIM](#)   [Book](#)

Search  for

☐ 1: AY109457. Zea mays CL12356\_...[gi:21213184]

[Links](#)

LOCUS AY109457 1349 bp mRNA linear HTC 17-OCT-2002  
 DEFINITION Zea mays CL12356\_1 mRNA sequence.  
 ACCESSION AY109457  
 VERSION AY109457.1 GI:21213184  
 KEYWORDS HTC.  
 SOURCE Zea mays  
 ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
 clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 1349)  
 AUTHORS Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,  
 Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.  
 TITLE Maize Mapping Project/DuPont Consensus Sequences for Design of  
 Overgo Probes

JOURNAL Unpublished (2002)  
 REFERENCE 2 (bases 1 to 1349)  
 AUTHORS Coe,E.H.  
 TITLE Direct Submission  
 JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of  
 Missouri, Columbia, MO 65211, USA

COMMENT If you are interested in getting corresponding physical clones,  
 these are publicly available from ZmDB and may be found by BLAST  
 searching at MSL, [maizemap.org](http://maizemap.org); ZmDB, [www.zmdb.iastate.edu](http://www.zmdb.iastate.edu); TIGR,  
[www.tigr.org](http://www.tigr.org); or NCBI, [www.ncbi.nlm.nih.gov](http://www.ncbi.nlm.nih.gov). When the source of the  
 maize cDNA sequences is either Virginia Walbot, Stanford or Pat  
 Schnable, Iowa State, then clones may be requested from ZmDB:  
[www.zmdb.iastate.edu](http://www.zmdb.iastate.edu).

FEATURES Location/Qualifiers  
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 /db\_xref="MaizeDB:630146"  
 /db\_xref="taxon:4577"  
 /clone\_lib="Maize Mapping Project/DuPont Consensus  
 Library"  
 /note="this sequence is part of a project of EST  
 assemblies resulting from the application of public  
 contigs to seed DuPont contigs; this resource was  
 assembled by DuPont as part of a collaboration for the  
 overgo addressing of BACs in conjunction with the Maize  
 Mapping Project"

BASE COUNT 350 a 314 c 286 g 310 t 89 others  
 ORIGIN

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1 aatgacatac catgcgtgac tcactctgctg cataacaaaa gcgcggtaca aaatggatag
61 cacgcgaact aaatcgga caaaactttg gcagtgtcac tgaaggaata caggagcatg
121 agactccgga tggctatttg tacatgtggt taaaggaaaa cagaaatcaa acgcataaga
181 ttgcactatg atctgaacct acaatgataa acacatctga ctgatcttta gcccttacag

```

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241 attttaaagt tgacttctaa aatgtacaat tgaagtcaga ggaaatatgg gactgcagtc
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361 atctttctcat cgaagcttaa tatagaagct acattgccac atctgtagca ataattgggt
421 gcagaccaca cagttacaag gcccttctcc tggaaacatgt actttaagcc ttcttgacc
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541 cgcgatccaa acagccaacc tgctccacgg ggactaacag cccatgtctc tatctcctca
601 gggtcactcc acataagatc gcagaaaggg .ccttcatggg gaatttcaca attgcgatca
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721 acttggccat taatgattgc tgatagcgta aggtaatcnn nnncatcagt gcaataccgc
781 catgcattgg cgttgccata cttcctctga cactcatcat agaaaccata cacctgtgtc
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901 agtagcaata ggatggtgaa aacctctaga ctattgaagc cacggtccac aaaatcacc
961 atgaaaatat agttcgtctc tgggacgtgg ccaccgctcg cgaagagctt cattaggtca
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1261 gaggaggaaa ccctctcctt gctattggcg gctccnnnnn nnnnnnnnnn nnnnnnnnnn
1321 nnnnnnnnnn nnnnnnnnnn ntggatgcg
```

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Revised: July 5, 2002.

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Dec 19 2002 15:44:50